Package ‘omicRexposome’

August 25, 2019

Title Exposome and omic data associatin and integration analysis

Version 1.6.0

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Description omicRexposome systematizes the association evaluation between exposures and omic data, taking advantage of MultiDataSet for coordinated data management, rexposome for exposome data definition and limma for association testing. Also to perform data integration mixing exposome and omic data using multi co-inherent analysis (omicade4) and multi-canonical correlation analysis (PMA).

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Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

VignetteBuilder knitr

Depends R (>= 3.4), Biobase

Imports stats, utils, grDevices, graphics, methods, rexposome, limma, sva, ggplot2, ggrepel, PMA, omicade4, gridExtra, MultiDataSet, SmartSVA, isva, parallel, SummarizedExperiment, stringr

Suggests BiocStyle, knitr, rmarkdown, snpStats, brgedata

biocViews ImmunoOncology, WorkflowStep, MultipleComparison, Visualization, GeneExpression, DifferentialExpression, DifferentialMethylation, GeneRegulation, Epigenetics, Proteomics, Transcriptomics, StatisticalMethod, Regression

git_url https://git.bioconductor.org/packages/omicRexposome
git_branch RELEASE_3_9
git_last_commit a6d6666
git_last_commit_date 2019-05-02

Date/Publication 2019-08-24

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**add_cls**

*Method to add an ExposomeClust to a MultiDataSet*

**Description**

This method allows to insert an object of class *ExposomeClust* as an independent dataset into an object of class *MultiDataSet*.

**Usage**

```r
add_cls(object, clsSet, ...)
```

```r
# S4 method for signature 'MultiDataSet,ExposomeClust'
add_cls(object, clsSet, ...)
```

**Arguments**

- **object**
  - An object of class *MultiDataSet*.

- **clsSet**
  - An object of class *ExposomeClust*.

- **...**
  - Arguments given to `add_eset` from *MultiDataSet*.

**Value**

A *MultiDataSet* with the *ExpressionSet* added as an independent dataset.
add_exp

Examples

data("eclust", package = "rexposome")
library(MultiDataSet)
md <- new("MultiDataSet")
names(md)
md <- add_cls(md, expo_c)
names(md)

add_exp

Method to add an ExposomeSet to a MultiDataSet

Description

This method allows to insert an object of class ExposomeSet as an independent dataset into an object of class MultiDataSet.

Usage

add_exp(object, expoSet, warnings = TRUE, ...)

## S4 method for signature 'MultiDataSet,ExposomeSet'
add_exp(object, expoSet, warnings = TRUE, ...

Arguments

object An object of class MultiDataSet.
expoSet An object of class ExposomeSet.
warnings (default TRUE) If set to FALSE warnings will not be displayed.
... Arguments given to add_eset from MultiDataSet.

Value

A MultiDataSet with the ExpressionSet added as an independent dataset.

Examples

data("exposome", package = "rexposome")
library(MultiDataSet)
md <- new("MultiDataSet")
names(md)
md <- add_exp(md, expo)
names(md)
association

asr ResultSet for testing and illustration purposes

Description

ResultSet created using association method, testing proteome association to exposome ("mds"), adjusted by sex and age.

Usage

data("asr")

Format

An object of class ResultSet of length 15.

Value

A ResultSet object.

Examples

data("asr", package = "omicRexposome")
asr

association # —————————————————————————– Method to perform an association study between transcriptome and exposom

Description

This function allows to perform an association study between gene expression from microarray and the exposome. An ExpressionSet is the object storing the gene expression and an ExposomeSet the one storing the exposome. Both of them needs to be encapsulated in a MultiDataSet. The association study is perform through standard limma pipeline. The function allows to perform multiple tests using the argument exposures.

Usage

association(object, formula, expset, omicset, set = "exposures", method = "ls", ..., baselevels, sva = "none", vfilter = NULL, verbose = FALSE, warnings = TRUE)

## S4 method for signature 'MultiDataSet'
association(object, formula, expset, omicset, set = "exposures", method = "ls", ..., baselevels, sva = "none", vfilter = NULL, verbose = FALSE, warnings = TRUE)
Arguments

object A MultiDataSet object containing at least one omic data-sets like ExpressionSet, MethylationSet... and, at last, one ExposomeSet.

formula formula to be evaluated by each exposure (or phenotype, see set argument). It should not contain any exposures (or phenotype), it will be added automatically when evaluated.

expset Name of the ExposomeSet in object.

omicset Name of the omic data-set in object.

set (default "exposures") Can take value "exposures" to test the association of the exposures in the ExposomeSet vs. the features in the omic data-set. If takes "phenotypes" all phenotypes in ExposomeSet are tested.

method (default "lm") Check limma help pages.

... Arguments passed to limma’s lmFit.

baselevels (optional) If set, must be a labeled vector with the default base level for categorical exposures.

sva (default "none"). This argument can take value "none" to do not apply SVA. Value "fast" will run SVA using isva and SmartSVA. Value "slow" will run SVA using sva.

vfilter (default NULL). Only used when sva = "slow". Numeric number of probes used in sva. Recommended ~10% of real probes.

verbose (default FALSE) If set to TRUE, a series of messages describing the process are shown.

warnings (default TRUE) If set to TRUE, a series of warnings are shown when required user attention.

Value

An object of class ResultSet.

Examples

library(MultiDataSet)
data(brge_prot, package = "brgedata")
data(brge_expo, package = "brgedata")
mds <- createMultiDataSet()
mds <- add_eset(mds, brge_prot, dataset.type = "proteines")
mds <- add_eset(mds, brge_expo, dataset.type = "exposures", GRanges = NA)
asr <- association(mds, formula = Asthma ~ Sex + Age,
                   expset = "exposures", omicset = "proteines")
asr
Function to perform a Transcriptome-Wide Association Study

Description

This function allows to perform a Transcriptome-Wide Association Study by using an ExposomeSet and an ExpressionSet. It allows to perform an adjustment using Surrogate Variable Analysis (from R package sva).

Usage

crossomics(object, method = "mcca", ncomponents = 2, ..., na.rm = FALSE, permute = c(100, 3), verbose = FALSE, warnings = TRUE)

Arguments

- object: A MultiDataSet object containing at least two data-sets like ExposomeSet, ExpressionSet, MethylationSet...
- method: (default "mcca") It can takes values "mcca" for Multiple Canonical Correlation Analysis or "mcia" for Multiple Co-Inertia Analysis.
- ncomponents: (default 2) Number of components to be estimated.
- ...: Other arguments given to mcia (from omicade4) or to MultiCCA (from PMA).
- na.rm: (default FALSE) If method was set to "mcca" and na.rm was set to TRUE, features containing missing values are removed.
- permute: (default c(100, 3)). If method="mcca" and this argument is set to NULL no permutation test to tune-up the parameters for MultiCCA. When filled, permute[1] corresponds to the number permutations (default in MultiCCA.permute is 25) and permute[2] the number of iterations (default in MultiCCA.permute is 3).
- verbose: (default FALSE) If set to TRUE, a series of messages describing the process are shown.
- warnings: (default TRUE) If set to TRUE, a series of warnings are shown when required user attention.

Value

An object of class ResultSet.

Examples

library(MultiDataSet)
library(rexposome)
data(brge_prot, package = "brgedata")
data(brge_expo, package = "brgedata")
mds <- createMultiDataSet()
mds <- add_eset(mds, brge_prot, dataset.type = "proteines")
crs <- add_eset(mds, imputation(brge_expo),
    dataset.type = "exposures", GRanges = NA)
crs <- crossomics(mds, method = "mcia")
crs

crs ResultSet for testing and illustration purposes

Description

ResultSet created using crossomics method, selecting "mcia" method. Result from the integration of proteome and exposome data ("mds").

Usage

data("crs")

Format

An object of class ResultSet of length 1.

Value

A ResultSet object.

Examples

data("crs", package = "omicExposome")
crs

getIntegration Method to extract integration-feature result from a ResultSet

Description

Homologous methods from MultiDataSet (getAssociation) but for ResultSet created by crossomics. It returns a data.frame with the result from mcia (omicade4) or from MultiCCA (PMA).

Usage

getIntegration(object, ...)

## S4 method for signature 'ResultSet'
getIntegration(object, ...)

Arguments

object An object of class ResultSet obtained from

... NOT USED
Value

A data.frame

Examples

data("crs", package = "omicRexposome")
class(getIntegration(crs))

mds  MultiDataSet for testing and illustration purposes

Description

MultiDataSet containing both proteome data-set and exposome data-set.

Usage

data("mds")

Format

An object of class MultiDataSet of length 2.

Value

A MultiDataSet object.

Examples

data("mds", package = "omicRexposome")
mds

omicRexposome: Package for exposome and omic data association and integration

Description

omicRexposome: Package for exposome and omic data association and integration

exposome-omic data association study

The packages offers the function `association` that allows to perform an association study using transcriptome, methylome, etc. as dependent variable and exposome data as independent variable. The function relies on `limma` pipeline and generates an object of class `ResultSet`, that can be plotted using `plotAssociation`.

exposome-omic data integration study

The packages offers the function `crossomics` that allows to perform two types of integration study: Multi Canonical Correlation Analysis and Multi Co-Inertia Analysis. The function allos to use any type and number of datasets (aka. exposome transcriptome, methylome, etc.). The function generates an object of class `ResultSet`, that can be plotted using `plotIntegration`. 
plotAssociation

Function to draw the result of an association study

Description

This function draws two types of plots for the ResultSet from association functions.

Usage

```r
plotAssociation(object, rid = 1, coef = 2, contrast = 1,
    type = c("manhattan", "qq", "volcano"), tPV = NULL, tFC = NULL,
    show.effect = FALSE)
```

## S4 method for signature 'ResultSet'

```r
plotAssociation(object, rid = 1, coef = 2,
    contrast = NULL, type = c("manhattan", "qq", "volcano"), tPV = NULL,
    tFC = NULL, show.effect = FALSE)
```

Arguments

- `object`: An object of class `ResultSet` obtained from `assoc_*` functions.
- `rid`: (default 1) Index or name of the test to be plotted.
- `coef`: (default 2) Index of the coefficient to be extracted.
- `contrast`: (default 1) When the code corresponds to a multicalourgical variable, contrast selects the comparison.
- `type`: Can take "volcano", "qq", "manhattan" and "protein". "protein" lot is a type of Manhattan plot designed for protein association analysis.
- `tPV`: (optional) Threshold for P.Value when type="volcano".
- `tFC`: (optional) Threshold for Fold Change or Effect when type="volcano".
- `show.effect`: (default FALSE) If set to TRUE, when type="volcano" the X-axis will show $2^{\log FC}$ instead of $\log FC$.

Value

A ggplot2 object.

See Also

`plotIntegration` for plotting integration results. `association` to create a ResultSet to be passed to this function.

Examples

```r
data("asr", package = "omicRexposome")
plotAssociation(asr, type = "qq")
plotAssociation(asr, type = "volcano")
```
plotHits

**Plot number of hits per result in ResultSet**

**Description**

This method draws a barplot with the number of hits in each result stored in the given ResultSet.

**Usage**

```r
plotHits(object, th = 0.05, width = 0.75)
```

### S4 method for signature 'ResultSet'

```r
plotHits(object, th = 0.05, width = 0.75)
```

**Arguments**

- `object`: An object of class `ResultSet`
- `th`: (default 0.05) Threshold (p-value) to consider a result as a hit.
- `width`: (default 0.70) width of the bar

**Value**

A ggplot2 object

**See Also**

- `plotLambda` for a graphical representation of the lambda score per analysis
- `tableLambda` for the lambda score per analysis
- `tableHits` for the hits per analysis

**Examples**

```r
data(asr, package = "omicRexposome")
plotHits(asr)
```

plotIntegration

**Function to draw de result of an integration study**

**Description**

This function draws plots for the ResultSet from integration function.

**Usage**

```r
plotIntegration(object, cmpX = 1, cmpY = 2, lb.th = 0.2,
        legend.show = TRUE, colors, ...)
```

### S4 method for signature 'ResultSet'

```r
plotIntegration(object, cmpX = 1, cmpY = 2,
        lb.th = 0.2, legend.show = TRUE, colors, ...)
```
plotLambda

Arguments

object An object of class ResultSet obtained from crossomics.
cmpX (default 1) Value of the X-axis when plotting results from mcia.
cmpY (default 2) Value of the Y-axis when plotting results from mcia.
lb.th (default 0.20) Threshold to place labels on radar chart drawn when plotting results from MultiCCA.
legend.show (default TRUE) If set to FALSE, right legend of radar plot is hidden when plotting results from MultiCCA.
colors (optional) Names vector with the colors used to draw each dataset. Used when plotting results from MultiCCA. If missing, random colors are chosen.
...

Optional arguments are given to plot from omicade4 package (argument axes is filled with values from cmpX and cmpY).

Value

A ggplot2 object

See Also

plotAssociation for plotting association results. crossomics to create a ResultSet to be passed to this function.

Examples

data("crs", package = "omicRexposome")
plotIntegration(crs)

plotLambda

Plot lambda score for all results in a ResultSet

Description

This method draws a barplot with the lambda score of each result in the given ResultSet.

Usage

plotLambda(object, width = 0.75)

# S4 method for signature 'ResultSet'
plotLambda(object, width = 0.75)

Arguments

object An object of class ResultSet
width (default 0.70) width of the bar

Value

A ggplot2 object
See Also

plotHits for a graphical representation of the hits per analysis, tableLambda for the lambda score per analysis, tableHits for the hits per analysis

Examples

data("asr", package = "omicReposome")
plotLambda(asr)

snpToContinuous

Transforms the discrete genotype from a snpSet to a matrix of a continuous variable.

Description

The function converts the categorical variable of SNPs to a continuous variable by normalizing each SNP as described in Abraham G. and Inouye M. 2014 (DOI: 10.1371/journal.pone.0093766).

Usage

snpToContinuous(snpSet, verbose = FALSE)

Arguments

snpSet An object of class snpSet with set calls slot.
verbose If set to TRUE, messages will be shown.

Value

An matrix of the calls of the SNPs converted to a continuous variable.

See Also
crossomics use this function

tableHits

Counts the number of hits on the results stored in a ResultSet

Description

Given a threshold it counts the number of hits in each result in the given ResultSet.

Usage

tableHits(object, th = 0.05)

## S4 method for signature 'ResultSet'
tableHits(object, th = 0.05)
**Arguments**

- **object** An object of class `ResultSet`  
  (default 0.05) Threshold (p-value) to consider a result as a hit.

**Value**

A labeled numeric vector with the exposures and the number of hits.

**See Also**

- `tableLambda` for the lambda score per analysis,  
- `plotLambda` for a graphical representation of the lambda score per analysis,  
- `plotHits` for a graphical representation of the hits per analysis

**Examples**

```r
data("asr", package = "omicRexposome")
tableLambda(asr)
```

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